CLAIMS

1. A GCRI polypeptide or a GCR2 polypeptide, or a fragment, homologue, variant or derivative thereof.

2. A polypeptide according to claim 1, which has at least 50% homology to a sequence shown in SEQ ID NO: 2.

3. The polypeptide of claim 2, which has at least 60% homology to a sequence shown in SEQ ID NO: 2.

4. The polypeptide of claim 3, which has at least 70% homology to a sequence shown in SEQ ID NO: 2.

5. The polypeptide of claim 4, which has at least 80% homology to a sequence shown in SEQ ID NO: 2.

6. The polypeptide of claim 5, which has at least 90% homology to a sequence shown in SEQ ID NO: 2.

7. The polypeptide of claim 6, which has at least 95% homology to a sequence shown in SEQ ID NO: 2.

8. A nucleic acid encoding a polypeptide according to claim 1, or a fragment, homologue, variant or derivative thereof.

9. A nucleic acid comprising a sequence of 25 contiguous nucleotides of the nucleic acid of claim 8.

10. A nucleic acid comprising a sequence of 15 contiguous nucleotides of the nucleic acid of claim 8.

11. A nucleic acid having at least 90% homology with the sequence set forth in SEQ ID NO: 1, or a fragment, variant or derivative thereof.

12. A nucleic acid comprising a sequence of 25 contiguous nucleotides of the nucleic acid of claim 11.

13. A nucleic acid comprising a sequence of 15 contiguous nucleotides of the nucleic acid of claim 11.

14. A nucleic acid having at least 75% homology with the sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 or SEQ ID NO: 9, or a fragment, variant or derivative thereof.

15. A nucleic acid comprising a sequence of 25 contiguous nucleotides of the nucleic acid according to claim 14.

16. A nucleic acid comprising a sequence of 15 contiguous nucleotides of the nucleic acid according to claim 14.

17. The complement of a nucleic acid sequence according to claim 8.

18. The complement of a nucleic acid sequence according to claim 11.

19. The complement of a nucleic acid sequence according to claim 14.

20. A nucleic acid according to claim 8, comprising one or more nucleotide substitutions, wherein such substitutions do not alter the coding specificity of said nucleic acid as a result of the degeneracy of the genetic code.

21. A nucleic acid according to claim 11, comprising one or more nucleotide substitutions, wherein such substitutions do not alter the coding specificity of said nucleic acid as a result of the degeneracy of the genetic code.

22. A nucleic acid according to claim 14, comprising one or more nucleotide substitutions, wherein such substitutions do not alter the coding specificity of said nucleic acid as a result of the degeneracy of the genetic code.

23. A polypeptide encoded by a nucleic acid according to claim 8.

24. A polypeptide encoded by a nucleic acid according to claim 11.

25. A polypeptide encoded by a nucleic acid according to claim 14.

26. A polypeptide according to claim 23, in which the polypeptide comprises a sequence shown in SEQ ID NO: 2 or SEQ ID NO: 4.

27. A polypeptide according to claim 24, in which the polypeptide comprises a sequence shown in SEQ ID NO: 2 or SEQ ID NO: 4.

28. A polypeptide according to claim 25, in which the polypeptide comprises a sequence shown in SEQ ID NO: 2 or SEQ ID NO: 4.

29. A method for identifying a pluripotent cell, comprising detecting the presence of a polypeptide according to claim 1 or a polypeptide encoded by a nucleic acid encoding a polypeptide according to claim 1, or a fragment, homologue, variant or derivative thereof, or the expression of a nucleic acid encoding a polypeptide according to claim 1, or a fragment, homologue, variant, homologue, or derivative thereof, or a nucleic acid having at least 90% homology with the sequence set forth in SEQ ID NO: 1, or a fragment, variant, homologue or derivative thereof, or a nucleic acid having at least 75% homology with the sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 or SEQ ID NO: 9, or a fragment, variant, homologue or derivative thereof.

30. A method according to claim 29, comprising the steps of amplifying nucleic acids from a putative pluripotent cell using 5' and 3' primers specific for GCRI and/or GCR2,

and detecting amplified nucleic acid thus produced.

31. A method according to claim 29, wherein the expression of the nucleic acid sequence is detected by in situ hybridisation.

32. A method according to claim 15, wherein the expression of the nucleic acid sequence is determined by detecting the protein product encoded thereby.

33. A method according to claim 29, wherein the protein product is detected by immunostaining.

34. A method according to claim 32, wherein the protein product is detected by immunostaining.

35. An antibody specific for a polypeptide according to claim 1, a polypeptide encoded by a nucleic acid encoding a polypeptide according to claim 1, or a fragment, homologue, variant or derivative thereof.

36. An antibody according to claim 35, which is capable of specifically binding to an extracellular domain of GCRl.

37. A method of using an antibody according to claim 35 for the identification and/ or isolation of a pluripotent cell.

38. A pluripotent cell identified by a method comprising detecting the presence of a polypeptide according to claim 1 or a polypeptide encoded by a nucleic acid encoding a GCRI polypeptide or a GCR2 polypeptide, or a fragment, homologue, variant or derivative thereof, or a fragment, homologue, variant or derivative thereof, or the expression of a nucleic acid encoding a GCRI polypeptide or a GCR2 polypeptide, or a fragment, homologue, variant or derivative thereof, or a fragment, homologue, variant, homologue, or derivative thereof, or a nucleic acid having at least 90% homology with the sequence set forth in SEQ ID NO: 1, or a fragment, variant, homologue or derivative thereof, or a nucleic acid having at least 75% homology with the sequence set forth in

SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 or SEQ ID NO: 9, or a fragment, variant, homologue or derivative thereof.

39. A pluripotent cell identified by a method of using an antibody according to claim 35 for the identification and/ or isolation of a pluripotent cell.

40. A method for isolating a gene specifically expressed in a pluripotent cell, comprising the steps of (a) providing a population of cells containing a pluripotent cell; (b) isolating one or more pluripotent cells therefrom and providing single-cell pluripotent cell isolates; (c) amplifying the transcribed nucleic acid present in a single pluripotent cell; (d) conducting a subtractive hybridisation screen to identify transcripts present in pluripotent cells but not in somatic cells; and (e) probing a nucleic acid library with one or more transcripts identified in (d) to clone one or more genes which are specifically expressed in pluripotent cells.

41. A method according to claim 29, in which the pluripotent cell is selected from the group consisting of a primordial germ cell (PGC), an embryonic stem cell (ES) and an embryonic germ cell (EG).

42. A method according to claim 33, in which the pluripotent cell is selected from the group consisting of a primordial germ cell (PGC), an embryonic stem cell (ES) and an embryonic germ cell (EG).

43. A method according to claim 37, in which the pluripotent cell is selected from the group consisting of a primordial germ cell (PGC), an embryonic stem cell (ES) and an embryonic germ cell (EG).

44. A method according to claim 40, in which the pluripotent cell is selected from the group consisting of a primordial germ cell (PGC), an embryonic stem cell (ES) and an embryonic germ cell (EG).

45. A pluripotent cell according to claim 40, in which the pluripotent cell is selected from the group consisting of a primordial germ cell (PGC), an embryonic stem cell (ES) and an embryonic germ cell (EG).

46. A transgenic non-human animal comprising a nucleic acid or the complement thereof, wherein the nucleic acid

encodes a polypeptide according to claim 1, or a fragment, homologue, variant or derivative thereof; or

has at least 90% homology with the sequence set forth in SEQ ID NO: 1, or a fragment, variant or derivative thereof; or

has at least 75% homology with the sequence set forth in SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8 or SEQ ID NO: 9, or a fragment, variant or derivative thereof.

47. The transgenic non-human animal according to claim 46, wherein the nucleic acid or complement thereof comprises one or more nucleotide substitutions, wherein such substitutions do not alter the coding specificity of said nucleic acid or complement thereof as a result of the degeneracy of the genetic code.

48. A transgenic non-human animal according to Claim 46 which is a mouse.

49. A cell or tissue from a transgenic non-human animal according to Claim 46.

50. Use of a transgenic non-human animal according to Claim 46, or a cell or tissue from a transgenic non-human animal according to Claim 46, in a method of identifying a compound which is capable of interacting specifically with a Stella or Fragilis protein.

51. A non-human transgenic animal, characterised in that the transgenic animal comprises an altered Stella gene or an altered Fragilis gene, or both.

52. A non-human transgenic animal according to Claim 51, in which the alteration is selected from the group consisting of: a deletion of Stella and/or Fragilis, a mutation in Stella and/or Fragilis resulting in loss of function, introduction of an exogenous gene

having a nucleotide sequence with targeted or random mutations into Stella and/or Fragilis, introduction of an exogenous gene from another species into Stella and/or Fragilis, and a combination of any of these.

53. A non-human transgenic animal having a functionally disrupted endogenous Stella and/or Fragilis gene, in which the transgenic animal preferably comprises in its genome and expresses a transgene encoding a heterologous Stella and/or Fragilis protein.

54. A nucleic acid construct for functionally disrupting a Stella and/or Fragilis gene in a host cell, the nucleic acid construct comprising: (a) a non-homologous replacement portion; (b) a first homology region located upstream of the non-homologous replacement portion, the first homology region having a nucleotide sequence with substantial identity to a first Stella and/or Fragilis gene sequence; and (c) a second homology region located downstream of the non-homologous replacement portion, the second homology region having a nucleotide sequence with substantial identity to a second Stella and/or Fragilis gene sequence, the second Stella and/or Fragilis gene sequence having a location downstream of the first Stella and/or Fragilis gene sequence in a naturally occurring endogenous Stella and/or Fragilis gene.